

Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

GTCGACCCACGCGTCCGCACTCAACAATGCCTGCCCTCTCTGACTGCACCGTCCCGCCGCGCTGCCGCCGCGCGCC	79
CAAGCCAAGTCGAGCGGGGGCGTTGCCACCGACGGCACAGCCCTTGGGGCCGCGCCGGGACCAGGAGGTGAGCCGCGCG	158
CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCCGCCAGGTGCCCGCAGCCCGCGCGCGAG	233
ATG CAC AGC CCG	4
P G L L A L W L C A V L C A S A R G G S	24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCT GTG CTG TGC GCA TCG GCG CGC GGG GGC AGC	293
D P Q P G P G R P A C P A P C H C Q E D	44
GAC CCC CAG CCT GGC CCG GGG CGT CCC GCC TGC CCG GCT CCC TGC CAC TGC CAG GAG GAC	353
G I M L S A D C S E L G L S V V P A D L	64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG	413
D P L T A Y L D L S M N N L T E L Q P G	84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT	473
L F H H L R F L E E L R L S G N H L S H	104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTG CGG CTC TCA GGG AAC CAC CTC TCA CAC	533
I P G Q A F S G L H S L K I L M L Q S N	124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC	593
Q L R G I P A E A L W E L P S L Q S L R	144
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC	653
L D A N L I S L V P E R S F E G L S S L	164
CTA GAT GCT AAT CTC ATC TCC CTG GTC CCT GAG AGA AGC TTT GAG GGG CTC TCC TCC CTC	713
R H L W L D D N A L T E I P V R A L N N	184
CGC CAC CTC TGG CTG GAT GAC AAT GCA CTC ACT GAG ATC CCC GTC AGA GCT CTC AAC AAC	773
L P A L Q A M T L A L N H I R H I P D Y	204
CTT CCT GCC CTA CAG GCC ATG ACC TTG GCT CTC AAC CAT ATC CGC CAC ATC CCT GAC TAT	833
A F Q N L T S L V V L H L H N N R I Q H	224
GCC TTC CAG AAC CTC ACC AGT CTT GTG GTG CTG CAT CTA CAT AAC AAC CGC ATC CAG CAT	893
V G T H S F E G L H N L E T L D L N Y N	244
GTG GGG ACC CAC AGC TTC GAG GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAC TAT AAT	953
E L Q E F P L A I R T L G R L Q E L G F	264
GAG CTG CAG GAG TTC CCC TTG GCT ATC CGG ACC CTG GGC AGG CTG CAG GAA TTG GGT TTC	1013
H N N N I K A I P E K A F M G N P L L Q	284
CAT AAC AAC AAC ATC AAG GCT ATC CCA GAG AAA GCC TTC ATG GGC AAC CCT CTC CTG CAG	1073
T I H F Y D N P I Q F V G R S A F Q Y L	304
ACA ATA CAT TTT TAT GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA GCA TTC CAG TAC CTG	1133
S K L H T L S L N G A T D I Q E F P D L	324
TCT AAA CTG CAT ACG CTA TCT TTG AAT GGT GCC ACT GAT ATC CAA GAG TTC CCA GAC CTC	1193
K G T T S L E I L T L T R A G I R L L P	344
AAA GGC ACC ACT AGC CTG GAG ATC CTG ACC CTG ACC CGT GCG GGC ATC AGA CTG CTC CCA	1253

Figure 1

L V V A G A Y I K L Y C D L P R G D F E 764
 CTG GTG GTG GCC GGC GCC TAC ATC AAG CTC TAC TGT GAC CTG CCA CGG GGT GAC TTT GAG 2513

 A V W D C A M V R H V A W L I F A D G L 784
 GCC GTG TGG GAC TGC GCC ATG GTG CGC CAC GTG GCC TGG CTC ATC TTT GCA GAT GGC CTC 2573

 L Y C P V A F L S F A S M L G L F P V T 804
 CTC TAC TGC CCC GTG GCC TTC CTC AGC TTT GCC TCC ATG CTG GGC CTC TTC CCT GTC ACC 2633

 P E A V K S V L L V V L P L P A C L N P 824
 CCC GAG GCT GTC AAG TCA GTC CTT CTG GTG GTG CTG CCT CTG CCT GCC TGC CTC AAC CCA 2693

 L L Y L L F N P H F R D D L R R L W P S 844
 CTG CTC TAC CTG CTC TTC AAC CCT CAC TTC CGG GAT GAC CTT CGG CGG CTC TGG CCA AGC 2753

 P R S F G P L A Y A A A G E L E K S S C 864
 CCT CGG TCC CCA GGG CCC CTA GCC TAC GCT GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC 2813

 D S T Q A L V A F S D V D L I L E A S E 884
 GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG 2873

 A G Q P P G L E T Y G F P S V T L I S R 904
 GCT GGG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA 2933

 H Q P G A T R L E G N H F I E S D G T K 924
 CAT CAG CCG GGG GCC ACC AGG CTG GAG GGA AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG 2993

 F G N P Q P P M K G E L L L K A E G A T 944
 TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG CTG AAG GCA GAG GGA GCC ACT 3053

 L A G C G S S V G G A L W P S G S L F A 964
 TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC 3113

 S H L * 968
 TCT CAC TTG TAA 3125

 ATATCCCTCTCTGTTTGTCTCTCCCCATCCAATGATGGCTGCTTATAAAAGAAAGACAACTCCAACCTCCATAGCAAGA 3204

 TGGCCAACACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTTGTCTTGG 3283

 CCTTCAGCTTCACTTTTACCCTGGGCTTCTCTGTCCAATCCAATACTTCTGACAGAGGCCTGGGAAATTTGCATAGGA 3362

 GAAAGGAGAAAAGCAAAGACAGTGAAGGTTATTGGGGCCCTGACAGAGCCATGATCAGTAAGTGCAGAGTGATGGGGAG 3441

 GTCTCACAGAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCTGTGACATATAGAATATAAAATG 3520

 TGTTCTGCGTTCCATTAACTTTGACCTATGCTGNGCCAAAGTGCTTCTGTATAAATACACTTTGGAAGACATTGAAAA 3599

 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637
 ??

Figure 1 (Cont'd)

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+LdLs N+Lt+l pg++++L+ LeeL Ls+N+L+++p ++f++L+

ftmzb048h1

67 LTAYLDLSMNNLTQLPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ L L+ N+L+++p++al+ Lp+L++L L+ N ++ +p+++f++L+

ftmzb048h1

115 SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L++L+L++N Lt++p al+nLp L+ L N+++++p+++fqnl+

ftmzb048h1

163 SLRHLWLDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNL 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+L+L nN+++++ +++++L+nLe+LdL++N+L+++p ++L+

ftmzb048h1

211 SLVVLHLHNNRIQHVGHHSFEGHLNLETDLNYNELQEFPL-AIRTLG 257

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+

ftmzb048h1

258 RLQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L++L+L++ +++++p+ l++ ++Le L L + ++ lppg++q L+

ftmzb048h1

306 KLHTLSLNGATdIQEFPD-LKGTTSLEILTLTRAGIRLLPPGVCQQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ L+Ls+N++++lp+ l+ +++Lee+ L +N+++++ ++f+ L+

ftmzb048h1

353 RLRILELSHNQIEELPS-LHRCQKLEEIGLRHNRKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L

ftmzb048h1

399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTPLAGLGGLM 446

Figure 2

Proteins with leucine-rich repeats

Protein (species) ^a	Function-ligand ^b	Location ^{a,b}	Repeats ^c	Length ^d	Consensus sequence ^e	PIR ^f entry
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm	15	28 (A) 29 (B)	.LE.L.L..C-.LT...C...aL... .L.EL.L..N..LGD.Ga..L...L.P..	A31857
Leucine-rich α2-GP (human)	?-?	Serum	8	24	.L.L.L.L..N..L..-L...LL...-	NBHUA2
RNA1 (<i>Saccharomyces cerevisiae</i>)	RNA processing-?	Cytoplasm	8	29	.L.L.L.L..N..a.....a.a.....	8VBYN1
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus	4	24	.L.L.L.a..N..a.....L...-	S03616
Biglycan (human)	ECM binding-laminin, fibronectin, TGF-β	ECM	8	24	.L.L.L.L..N..I...-a.....a.....	A40757
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF-β	ECM	10	24	.L.L.L.L..N..I...-V....a.....	NBHUC8
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM	11	24	.L.L.L.L..N..a...-a....a.....	S05390
Lumican (chicken)	Corneal transparency-?	ECM	12	24	.L.L.L.L..N..L...-....a.....	A41748
Proteoglycan-Lb (chicken)	?-?	ECM	6	24	.L..a.L..N..I...-....a.....	A41781
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM	6	24	.L..a.L..N..a...-....F.....	A35272
Platelet GP Iba (human)	Cell adhesion-vWF, thrombin	PM (EC)	7	24	.L.L.L.L..N..L...-LP.GL...L...-	NBHUA
Platelet GP V (human)	Cell adhesion-GP IX, GP Ib	PM (EC)	14	24	.L.L.L.L..N..L...-LP..LF...L...-	-
YopM (<i>Yersinia pestis</i>)	Virulence factor-thrombin	IC + EC	12	20	.L.L.L.a..N..L...-LP...-L-PP	A33950
IpaH7.8 (<i>Shigella flexneri</i>)	?-?	?	6	20	.L.L.L.V..N..L...-LP...-L-P..	A35149
IpaH4.5 (<i>Shigella flexneri</i>)	?-?	?	8	20	.L.L.L.a..N..L...-LP...-L-P..	S18248
Toll (<i>Drosophila</i>)	Embryo development-?	PM (EC)	19	24	.L.L.L.L..N..L...-....F.....	A29943
SIR (<i>Drosophila</i>)	Axon development-?	EC	19	24	.L.L.L.L..N..I...-....F..L...-	A36665
Connectin (<i>Drosophila</i>)	Synapse development-?	PM (EC)	7	24	.L.L.L.L..N..I...-....aF..L...-	S28464
Chaoptin (<i>Drosophila</i>)	Photoreceptor-cell development-?	PM (EC)	30	24	.L.L.L.L..N..a...-....F..a...-	A29944
Flightless-I (<i>Drosophila</i>)	Embryo development-?	PM (EC)	16	23	.L.L.L.L.S.N..L...-aP..a...L...-	-
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)	8	24	.L.L.L.L.S.N..a...-....L...-	A34210
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)	8	27	.a...L.L..N..-.....	TDHUM4
Trk (human)	Receptor protein kinase-NGF	PM (EC)	2	23	.L.L.L.L.S.N..L...-.....	TVHUTT
TrkB (mouse)	Receptor protein kinase-BDNF, NT-3	PM (EC)	3	23	.L.L.L.a.T.N..LTS...-.....T	S06943
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)	3	23	.LR.a.NLSQN..L...S...-.....	A40026
TMK1 (<i>Arabidopsis thaliana</i>)	Receptor protein kinase-?	PM (EC)	11	23	.L..a.L..N...G.aP...-a.SL...-	JQ1674
LHCG receptor (rat)	Signal transduction-LH, CG	PM (EC)	5	25	.L.L.L.a..T..a.....F.....	A41343
FSH receptor (rat)	Signal transduction-FSH	PM (EC)	7	25	.L.L.L.a.S.T...LP...a.a...-	A34548
TSH receptor (dog)	Signal transduction-TSH	PM (EC)	6	25	.a.L.L.a.NN..a.S-a.....a.....	A40077
Adenylate cyclase (<i>Saccharomyces cerevisiae</i>)	Signal transduction-RAS	PM (cytoplasm)	20	23	.L.L.L.L..N..a...-....a.L...-	OYBY
T-LR (<i>Trypanosoma brucei</i>)	?-?	?	18	23	.L.L.L.LSGC..a...-a...a.L...-	A36359
RAD1 (<i>Saccharomyces cerevisiae</i>)	DNA repair-RAD10	Nucleus	3	23	.a.LaDI..N..LP..a.....N...-	DDBYD1
RAD7 (<i>Saccharomyces cerevisiae</i>)	DNA repair-?	?	5	26	.L.L.L.a..C..a.....a.....P	A25226
DRT100 (<i>Arabidopsis thaliana</i>)	Recombination-?	Chloroplast	5	24	.L.L.L.L..N..L.G.IP.S-a.S...-	A46260
GRR1 (<i>Saccharomyces cerevisiae</i>)	Signal transduction-?	Cytoplasm	9	26	.L..a.L..C.NaTD..a...L..L...-	A41529
CCR4 (<i>Saccharomyces cerevisiae</i>)	Transcription-?	?	4	23	.L.L.L.a..N..LT..LP.E-a.....	S31286
sds22 (<i>Schizosaccharomyces pombe</i>)	Mitosis-dis2, sds21	Nucleus	11	22	.L.L.L.a..N..I...-a-Ena..L...-	A38439
p34 ribosome-binding protein (rat)	RM membranes-ribosome	RM membrane (cytoplasm)	4	24	.L.L.LDL..N..L...-LP...F..L...-	-
Carboxypeptidase N (human)	Stabilization-catalytic subunit	Plasma	12	24	.L.L.L.L..N..L...-LP..aF..L...-	A34901
Intestinalin (<i>Listeria monocytogenes</i>)	Invasion-?	Cell wall	13	22	NL...L.L..N-QISDI.P---L..L-T	A39930
IntB (<i>Listeria monocytogenes</i>)	?-?	?	6	22	.L.L.L.L..N..L.DI...-L..L...-	C39930
LRR superfamily					5 10 15 20 25 .L.L.L.L..N..a...a*****a***a...	

Figure 3

[illegible]

Figure 4

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[illegible]

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11

*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnl

+L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp ++L

fahr 64 SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTPLAGLGGL 110

k<*

fahr 111 M 111

Figure 6

1 MISPPGLIALMLCAVLCSARQGSDFQGGPACPAFCPCQEDGMLSDCSEGLSVVPAOLDFLTAYLILSBNLITE 160

81 LQGLFHEIRPLEIRLSGNHLSHTPGQAFSGLSHSLKILMLQSNQAGIPAEALNELPSLOSLRLDANLISLWPERSPFG 160

161 LSSLRHMLDDNALTRIPVRALELPALOANTLALNHIRHPDYAFQNLTSLVVILHBNRIQHVGHHSFEGRLNLSILA 240

241 LMYNELQEFPLAIRTLGRILQELCPHBNIDKATPECAFHGNHLLQTHFYDNPITQFVGRSAFYLSLHATLSNAGATOIQE 320

HTHYRES WYACKURS GJRGST

321 FFOLEGTTSLEYTLTRAGIRLLPFGVOOQLFRLRILELSHNOISELPSLHRCQKLESTGRHNRIDKEIGADTFSQLGSL 400

H-ASVE RSQGLSLF AHPASLAALASNTYASG KLEK DTSQSLSS

401 QALDLSMAIRAIHPEAFSTILSLVKLDLTDNQUTTLPLAGLOGMLHKLKGNLALSQAFSKDSFKRLRILEVFPAYQCC 480

MLKLEGNLALSQAFSKDSFKRLRILEVFPAYQCC

QALDLSMAIRSDHPEAFSTILSLVKLDLTDNQUTTLPLAGLOGMLHKLKGNLALSQAFSKDSFKRLRILEVFPAYQCC 480

481 AYGICASFYKTSQQAEDFHPPEEEAPKRPILGLLAGOAEHYDLDLDELQMGTEOSKPNPSVQCSPIVGGPFKPCHELFE 560

AYGICASFYKTSQQAEDFHPPEEEAPKRPILGLLAGOAEHYDLDLDELQMGTEOSKPNPSVQCSPIVGGPFKPCHELFE

FYGCASFYKASQQAEDLHLDDESSKRPILGLLAGOAEHYDLDLDELQMGTEOSKPNPSVQCSPTFGPFKPCHELFE 560

641 SMGIRLAWAIVLLSVLONGLVLLTVFASGSPSPVVKLVVGNAGANALTGISOGILLASVDALTYQQAFCYARWESGL 720

SMGIRLAWAIVLLSVLONGLVLLTVFASGSPSPVVKLVVGNAGANALTGISOGILLASVDALTYQQAFCYARWESGL

SMGIRLAWAIVLLSVLONGLVLLTVFASGSPSPVVKLVVGNAGANALTGISOGILLASVDALTYQQAFCYARWESGL 720

641 I TM II

GOQATGFLAVLGSEASVLLTLAAVQCSISVTCVRAYGKAESPGSVRAGALGCLALAGLAALPLASVGEYGAFLCLFY

GOQATGFLAVLGSEASVLLTLAAVQCSISVTCVRAYGKAESPGSVRAGALGCLALAGLAALPLASVGEYGAFLCLFY

GCRATGFLAVLGSEASVLLTLAAVQCSVSVSCVRAYGKSPSLGSGVRLGCLALAGLAALPLASVGEYGAFLCLFY

TM III TM IV

721 APPEGRPALGFAVALVHNSLCFLVWAGAYIKLYCOLPRGDFZAVHDCANVHVHMLITFADGLLYCPVAFLSFASHIGL 800

APPEGRPALGFAVALVHNSLCFLVWAGAYIKLYCOLPRGDFZAVHDCANVHVHMLITFADGLLYCPVAFLSFASHIGL

APPEGRPALGFAVALVHNSLCFLVWAGAYIKLYCOLPRGDFZAVHDCANVHVHMLITFADGLLYCPVAFLSFASHIGL 800

801 TMV TMVI

FPVTEAVKSVLLVWFLPACINELLYLLEHNFHFDLRLHPSPRSPGPLAYAANGELEKSSCDSTQALVAFSDVLDLIL

FPVTEAVKSVLLVWFLPACINELLYLLEHNFHFDLRLHPSPRSPGPLAYAANGELEKSSCDSTQALVAFSDVLDLIL

FPVTEAVKSVLLVWFLPACINELLYLLEHNFHFDLRLHPSPRSPGPLAYAANGELEKSSCDSTQALVAFSDVLDLIL 880

881 TM VI

EASEAQPPGLEYTGFPVTLISKHQPGATRLBQHIFVESDGTGFGNPOFFHIGELLKAEGATLAGOQSSVGGALNPSG

EASEAQPPGLEYTGFPVTLISKHQPGATRLBQHIFVESDGTGFGNPOFFHIGELLKAEGATLAGOQSSVGGALNPSG

EASEAQPPGLEYTGFPVTLISQOQPGAPRLBQSHVEPEGRHFGNPOFFHIGELLKAEGSTPAGOGI SOOQGFQPSG 960

961 968

SLFASHLN

SLFASHLN

LAFASHVN

Figure 7

G	L	H	N	L	E	T	L	D	L	N	Y	N	K	L	Q	E	F	P	V	20
GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAT	TAT	AAC	AAG	CTG	CAG	GAG	TTC	CCT	GTG	60
A	I	R	T	L	G	R	L	Q	E	L	G	F	H	N	N	N	I	K	A	40
GCC	ATC	CGG	ACC	CTG	GGC	AGA	CTG	CAG	GAA	CTG	GGG	TTC	CAT	AAC	AAC	AAC	ATC	AAG	GCC	120
I	P	E	K	A	F	M	G	N	P	L	L	Q	T	I	H	F	Y	D	N	60
ATC	CCA	GAA	AAG	GCC	TTC	ATG	GGG	AAC	CCT	CTG	CTA	CAG	ACG	ATA	CAC	TTT	TAT	GAT	AAC	180
P	I	Q	F	V	G	R	S	A	F	Q	Y	L	P	K	L	H	T	L	S	80
CCA	ATC	CAG	TTT	GTG	GGA	AGA	TCG	GCA	TTC	CAG	TAC	CTG	CCT	AAA	CTC	CAC	ACA	CTA	TCT	240
L	N	G	A	M	D	I	Q	E	F	P	D	L	K	G	T	T	S	L	E	100
CTG	AAT	GGT	GCC	ATG	GAC	ATC	CAG	GAG	TTT	CCA	GAT	CTC	AAA	GGC	ACC	ACC	AGC	CTG	GAG	300
I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	L	120
ATC	CTG	ACC	CTG	ACC	CGC	GCA	GGC	ATC	CGG	CTG	CTC	CCA	TCG	GGG	ATG	TGC	CAA	CAG	CTG	360
P	R	L	R	V	L	E	L	S	H	N	Q	I	E	E	L	P	S	L	H	140
CCC	AGG	CTC	CGA	GTC	CTG	GAA	CTG	TCT	CAC	AAT	CAA	ATT	GAG	GAG	CTG	CCC	AGC	CTG	CAC	420
R	C	Q	K	L	E	E	I	G	L	Q	H	N	R	I	W	E	I	G	A	160
AGG	TGT	CAG	AAA	TTG	GAG	GAA	ATC	GGC	CTC	CAA	CAC	AAC	CGC	ATC	TGG	GAA	ATT	GGA	GCT	480
D	T	F	S	Q	L	S	S	L	Q	A	L	D	L	S	W	N	A	I	R	180
GAC	ACC	TTC	AGC	CAG	CTG	AGC	TCC	CTG	CAA	GCC	CTG	GAT	CTT	AGC	TGG	AAC	GCC	ATC	CGG	540
S	I	H	P	E	A	F	S	T	L	H	S	L	V	K	L	D	L	T	D	200
TCC	ATC	CAC	CCT	GAG	GCC	TTC	TCC	ACC	CTG	CAC	TCC	CTG	GTC	AAG	CTG	GAC	CTG	ACA	GAC	600
N	Q	L	T	T	L	P	L	A	G	L	G	G	L	M	H	L	K	L	K	220
AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGA	CTT	GGG	GGC	TTG	ATG	CAT	CTG	AAG	CTC	AAA	660
G	N	L	A	L	S	Q	A	F	S	K	D	S	F	P	K	L	R	I	L	240
GGG	AAC	CTT	GCT	CTC	TCC	CAG	GCC	TTC	TCC	AAG	GAC	AGT	TTC	CCA	AAA	CTG	AGG	ATC	CTG	720
E	V	P	Y	A	Y	Q	C	C	P	Y	G	M	C	A	S	F	F	K	A	260
GAG	GTG	CCT	TAT	GCC	TAC	CAG	TGC	TGT	CCC	TAT	GGG	ATG	TGT	GCC	AGC	TTC	TTC	AAG	GCC	780
S	G	Q	W	E	A	E	D	L	H	L	D	D	E	E	S	S	K	R	P	280
TCT	GGG	CAG	TGG	GAG	GCT	GAA	GAC	CTT	CAC	CTT	GAT	GAT	GAG	GAG	TCT	TCA	AAA	AGG	CCC	840
L	G	L	L	A	R	Q	A	E	N	H	Y	D	Q	D	L	D	E	L	Q	300
CTG	GGC	CTC	CTT	GCC	AGA	CAA	GCA	GAG	AAC	CAC	TAT	GAC	CAG	GAC	CTG	GAT	GAG	CTC	CAG	900
L	E	M	E	D	S	K	P	H	P	S	V	Q	C	S	P	T	P	G	P	320
CTG	GAG	ATG	GAG	GAC	TCA	AAG	CCA	CAC	CCC	AGT	GTC	CAG	TGT	AGC	CCT	ACT	CCA	GGC	CCC	960
F	K	P	C	E	Y	L	F	E	S	W	G	I	R	L	A	V	W	A	I	340
TTC	AAG	CCC	TGT	GAG	TAC	CTC	TTT	GAA	AGC	TGG	GGC	ATC	CGC	CTG	GCC	GTG	TGG	GCC	ATC	1020
V	L	L	S	V	L	C	N	G	L	V	L	L	T	V	F	A	G	G	P	360
GTG	TTG	CTC	TCC	GTG	CTC	TGC	AAT	GGA	CTG	GTG	CTG	CTG	ACC	GTG	TTC	GCT	GGC	GGG	CCT	1080
A	P	L	P	P	V	K	F	V	V	G	A	I	A	G	A	N	T	L	T	380
GCC	CCC	CTG	CCC	CCG	GTC	AAG	TTT	GTG	GTA	GGT	GCG	ATT	GCA	GGC	GCC	AAC	ACC	TTG	ACT	1140

FIGURE 8

G	I	S	C	G	L	L	A	S	V	D	A	L	T	F	G	Q	F	S	E	400
GGC	ATT	TCC	TGT	GGC	CTT	CTA	GCC	TCA	GTC	GAT	GCC	CTG	ACC	TTT	GGT	CAG	TTC	TCT	GAG	1200
Y	G	A	R	W	E	T	G	L	G	C	R	A	T	G	F	L	A	V	L	420
TAC	GGA	GCC	CGC	TGG	GAG	ACG	GGG	CTA	GGC	TGC	CGG	GCC	ACT	GGC	TTC	CTG	GCA	GTA	CTT	1260
G	S	E	A	S	V	L	L	L	T	L	A	A	V	Q	C	S	V	S	V	440
GGG	TCG	GAG	GCA	TCG	GTG	CTG	CTG	CTC	ACT	CTG	GCC	GCA	GTG	CAG	TGC	AGC	GTC	TCC	GTC	1320
S	C	V	R	A	Y	G	K	S	P	S	L	G	S	V	R	A	G	V	L	460
TCC	TGT	GTC	CGG	GCC	TAT	GGG	AAG	TCC	CCC	TCC	CTG	GGC	AGC	GTT	CGA	GCA	GGG	GTC	CTA	1380
G	C	L	A	L	A	G	L	A	A	A	L	P	L	A	S	V	G	E	Y	480
GGC	TGC	CTG	GCA	CTG	GCA	GGG	CTG	GCC	GCC	GCA	CTG	CCC	CTG	GCC	TCA	GTG	GGA	GAA	TAC	1440
G	A	S	P	L	C	L	P	Y	A	P	P	E	G	Q	P	A	A	L	G	500
GGG	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCG	CCA	CCT	GAG	GGT	CAG	CCA	GCA	GCC	CTG	GGC	1500
F	T	V	A	L	V	M	M	N	S	F	C	F	L	V	V	A	G	A	Y	520
TTC	ACC	GTG	GCC	CTG	GTG	ATG	ATG	AAC	TCC	TTC	TGT	TTC	CTG	GTC	GTG	GCC	GGT	GCC	TAC	1560
I	K	L	Y	C	D	L	P	R	G	D	F	E	A	V	W	D	C	A	M	540
ATC	AAA	CTG	TAC	TGT	GAC	CTG	CCG	CGG	GGC	GAC	TTT	GAG	GCC	GTG	TGG	GAC	TGC	GCC	ATG	1620
V	R	H	V	A	W	L	I	F	A	D	G	L	L	Y	C	P	V	A	F	560
GTG	AGG	CAC	GTG	GCC	TGG	CTC	ATC	TTC	GCA	GAC	GGG	CTC	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680
L	S	F	A	S	M	L	G	L	F	P	V	T	P	E	A	V	K	S	V	580
GTC	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG	CCC	GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P	L	L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGC	CTC	AAC	CCA	CTG	CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	1860
A	Y	A	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	P	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG	CCC	CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	P	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CAG	CCA	GGG	GCC	CCC	AGG	2040
L	E	G	S	H	C	V	E	P	E	G	N	H	F	G	N	P	Q	P	S	700
CTG	GAG	GGC	AGC	CAT	TGT	GTA	GAG	CCA	GAG	GGG	AAC	CAC	TTT	GGG	AAC	CCC	CAA	CCC	TCC	2100
M	D	G	E	L	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720
ATG	GAT	GGA	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTG	TCA	2160
G	G	G	G	F	Q	P	S	G	L	A	F	A	S	H	V	*				737
GGG	GGT	GGC	GGC	TTT	CAG	CCC	TCT	GGC	TTG	GCC	TTT	GCT	TCA	CAC	GTG	TAA				2211
ATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACA	2290																			
AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGA	2369																			
CCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTCCTTG	2448																			
TCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGG	2527																			

FIGURE 8

CONT.

FIGURE 8
CONT.

100000 3634300

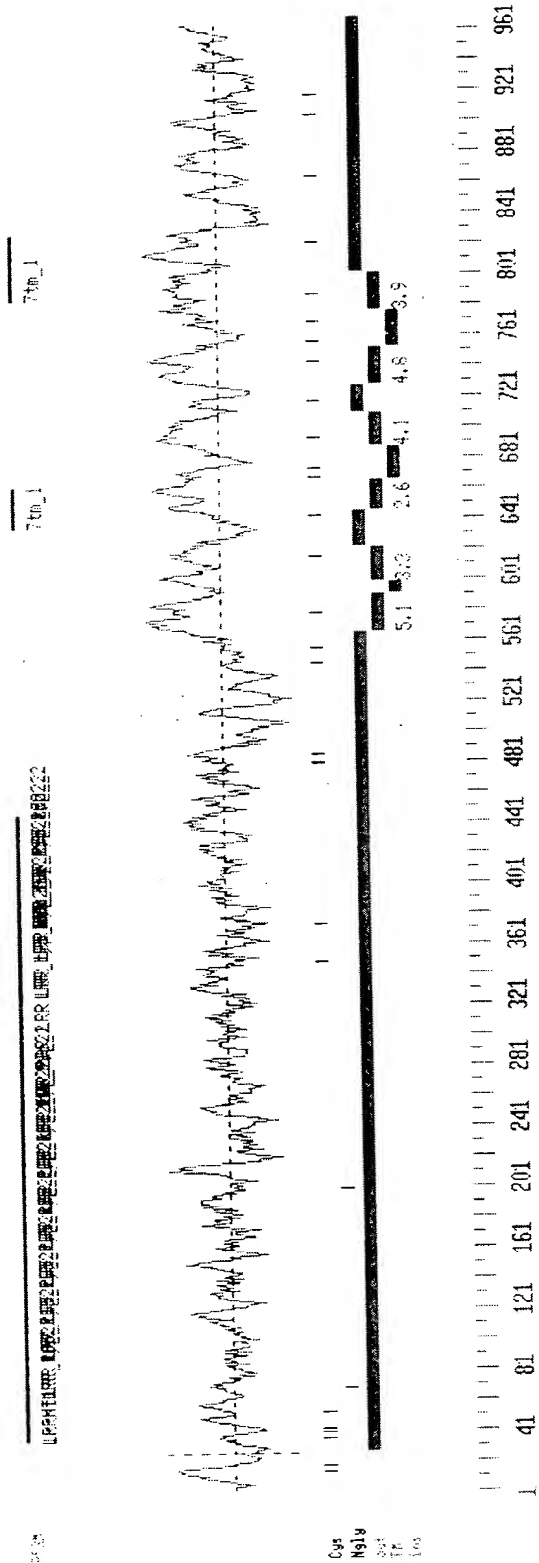


FIGURE 9

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR	Leucine Rich Repeat	241.4	1.3e-68	16
LRRNT	Leucine rich repeat N-terminal domain	27.2	0.00038	1
7tm_1	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
LRRNT	1/1	34	65..	1	31 []	27.2	0.00038
LRR	1/16	67	90..	1	23 []	12.4	11
LRR	2/16	91	114..	1	23 []	24.2	0.0031
LRR	3/16	115	138..	1	23 []	19.9	0.062
LRR	4/16	139	162..	1	23 []	16.4	0.7
LRR	5/16	163	186..	1	23 []	27.5	0.00031
LRR	6/16	187	210..	1	23 []	12.1	13
LRR	7/16	211	234..	1	23 []	21.6	0.019
LRR	8/16	235	257..	1	23 []	18.2	0.2
LRR	9/16	258	281..	1	23 []	19.0	0.11
LRR	10/16	282	305..	1	23 []	10.2	32
LRR	11/16	306	328..	1	23 []	5.6	1.5e+02
LRR	12/16	329	352..	1	23 []	8.8	52
LRR	13/16	353	374..	1	23 []	19.2	0.097
LRR	14/16	375	398..	1	23 []	16.9	0.49
LRR	15/16	399	422..	1	23 []	23.7	0.0042
LRR	16/16	423	446..	1	23 []	16.4	0.66
7tm_1	1/2	635	662..	51	79..	3.4	2.2
7tm_1	2/2	784	827..	207	259..	1.1	11

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038
 ->aCpreCtCsp..fglvVdCsgrgLtleVPrdIP<-
 aCp++C+C+++I+dCs++gL+vPdl
 15088 34 ACPAPCHCQEgIMLSADCSLGLS-AVPGDLD 65

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11
 ->nLeeLdLsnN.LtSlppglfsnLp<-
 +LdLsN+Lt+lpglft++L+
 15088 67 LTAYLDLSMNnLTELQPLFHHLR 90

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031
 ->nLeeLdLsnN.LtSlppglfsnLp<-
 LeeL+Ls+N+L+++p+fs+L
 15088 91 FLEELRLSGNhLSHIPGQAFSGLY 114

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062
 ->nLeeLdLsnN.LtSlppglfsnLp<-
 +L+L L+nN+L++p+++Lp
 15088 115 SLKILMLQNNqLGGIPAEALWELP 138

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7
 ->nLeeLdLsnN.LtSlppglfsnLp<-
 +L++L+L+N++p++f++L+
 15088 139 SLQSLRLDANIISLVPERSEGLS 162

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031
 ->nLeeLdLsnN.LtSlppglfsnLp<-
 +L++L+L++N.Lt++p+++nLp

FIGURE 10

15088 163 SLRHLWLDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13
 ->nLeeLdLsnN.LtslppglfsnLp<-
 L+ L N++++p+ +f+nL+
 15088 187 ALQAMTLALNriSHIPDYAFQNLT 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L +L+L+nN++++l ++f++L
 15088 211 SLVVHLHLHNNrIQHLGTHSFEGH 234

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2
 ->nLeeLdLsnN.LtslppglfsnLp<-
 nLe+LdL++N+L+++p +++ L
 15088 235 NLETDLNLYNkLQEFV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L+eL ++nN+++ +p+++f+ p
 15088 258 RLQELGFHNNnKAIPEKAFMGNP 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32
 ->nLeeLdLsnN.LtslppglfsnLp<-
 L++++ +N+++ + +f+ Lp
 15088 282 LLQTIHFYDNpIQFVGRSAFYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L+L++ +++++p+ +++ +
 15088 306 KLHTLSLNGAmdIQEFPD--LKGTT 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +Le L L + +++ lp+g +++Lp
 15088 329 SLEILTLTRAgIRLLPSGMCQQLP 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L Ls+N++++lp+ ++ ++
 15088 353 RLRVLELSHNqIEELPS--LHRCQ 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +Lee+ L++N+++ ++fs+L+
 15088 375 KLEEIGLQHNrWEIGADTFSQLS 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L+ LdLs N ++s+++p++fs L
 15088 399 SLQALDLSWNaIRSIHPEAFSTLH 422

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L +LdL +N+L+lp ++L
 15088 423 SLVKLDLTDNqLTTLPLAGLGGLM 446

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2
 ->dWpfGsalCklvtaldvvnmyaSillLta<-
 +W G ++C+ +++l v+ + aS+lLl+
 15088 635 RWETG-LGCRATGFLAVLGSEASVLLLT 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11
 *->ICWIPyfiVlIdtlc.IsiimsstCelervlptalvtwLayvNs
 l+ P +++ +l ++ ++++++v l++ ++
 15088 784 LLYCPVAFLSFASMLGIFPV-----TPEAVKSVLLVVLPLPA 820

cINPiY<-*
 cINP++Y
 15088 821 CLNPLLY 827

FIGURE 10 cont.

```
//
Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
```

```
-----
HMM file:          /ddm/robison/smart/smart/smart.all.hmms
Sequence file:     /prod/ddm/wspace/orfanal/oa-script.12184.seq
-----
```

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrntl		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
lrrntl	1/1	34	70	1	38	25.7	0.0011
LRR_PS_2	1/13	64	87	1	24	1.9	1.2e+02
LRR_typ_2	1/14	64	88	1	24	12.6	2.1
LRR_bac_2	1/7	89	108	1	20	0.9	80
LRR_PS_2	2/13	89	111	1	24	17.2	0.4
LRR_typ_2	2/14	89	112	1	24	32.1	1.3e-05
LRR_RI_2	1/4	89	115	1	28	3.6	14
LRR_bac_2	2/7	113	132	1	20	1.6	66
LRR_PS_2	3/13	113	136	1	24	1.1	1.5e+02
LRR_typ_2	3/14	113	136	1	24	19.2	0.1
LRR_bac_2	3/7	137	156	1	20	0.1	1e+02
LRR_PS_2	4/13	137	159	1	24	7.1	24
LRR_typ_2	4/14	137	160	1	24	25.9	0.00095
LRR_PS_2	5/13	161	183	1	24	11.4	6.6
LRR_typ_2	5/14	161	184	1	24	27.5	0.00031
LRR_sd22_2	1/5	161	187	1	22	5.3	31
LRR_RI_2	2/4	161	190	1	28	5.3	8
LRR_PS_2	6/13	185	207	1	24	7.0	25
LRR_typ_2	6/14	185	208	1	24	23.2	0.0062
LRR_PS_2	7/13	209	232	1	24	3.1	79
LRR_typ_2	7/14	209	232	1	24	28.1	0.0002
LRR_RI_2	3/4	209	235	1	28	1.2	31
LRR_sd22_2	2/5	209	235	1	22	13.5	3
LRR_bac_2	4/7	233	252	1	20	10.7	4.1
LRR_typ_2	8/14	233	255	1	24	16.1	0.76
LRR_PS_2	8/13	233	255	1	24	17.1	0.43
LRR_bac_2	5/7	256	275	1	20	0.2	1e+02
LRR_PS_2	9/13	256	278	1	24	2.9	85
LRR_typ_2	9/14	256	279	1	24	24.4	0.0026
LRR_typ_2	10/14	327	350	1	24	3.1	29
LRR_bac_2	6/7	351	370	1	20	14.6	1.3
LRR_PS_2	10/13	351	372	1	24	10.8	8
LRR_sd22_2	3/5	351	372	1	22	7.6	16
LRR_typ_2	11/14	351	373	1	24	18.8	0.13
LRR_RI_2	4/4	351	378	1	28	2.6	19
LRR_PS_2	11/13	373	396	1	24	2.3	1e+02
LRR_typ_2	12/14	374	396	1	24	6.8	10
LRR_sd22_2	4/5	397	418	1	22	7.0	19
LRR_PS_2	12/13	397	419	1	24	13.6	3.4
LRR_typ_2	13/14	397	420	1	24	30.4	4.3e-05
LRR_bac_2	7/7	421	440	1	20	5.8	18
LRR_sd22_2	5/5	421	441	1	22	3.7	49
LRR_PS_2	13/13	421	442	1	24	5.5	39
LRR_typ_2	14/14	421	444	1	24	21.6	0.018

Alignments of top-scoring domains:

FIGURE 11

lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
 ->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-
 +CPapC+C ++ ++ dCs++gL +vP dl + t +
 15088 34 ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLDP LTAY 70

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
 ->LtsL.qvLdLsnNnLsGeIPsslgn<-
 L L+ +LdLs NnL+ e+ + l+
 15088 64 LDPLtAYLDLSMNNLT-ELQPGLFH 87

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
 ->LpnL.reLdLsnNqLtsLPpgaFgg<-
 L L+ LdLs N+Lt+L pg+F++
 15088 64 LDPLtAYLDLSMNNLTTELQPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
 ->PpsLkeLnvsnNrLteLPeL<-
 +LeL+ s+N+L+ P
 15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+ L++L+Ls+N+Ls +IP + ++
 15088 89 LRFLEELRLSGNHLs-HIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 L+ L+eL+Ls+N+L+++P +aF+g
 15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
 ->npsLreLdLsnNkl.gdeGaraLaeaLks<-
 ++ L+eL+Ls+N+L+++ G + ++L s
 15088 89 LRFLEELRLSGNHLSHIPG--QAFSGLYS 115

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
 ->PpsLkeLnvsnNrLteLPeL<-
 sLk+L +nN+L P+
 15088 113 LYSLKILMLQNNQLGGIPAE 132

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L sL++L L+nN+L G + l+
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 L +L+ L L+nNqL +P++a++
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
 ->PpsLkeLnvsnNrLteLPeL<-
 psL++L+ + N ++ Pe
 15088 137 LPSLQSLRLDANLISLVPER 156

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq+L+L N +s +P+ +
 15088 137 LPSLQSLRLDANLIS-LVPERSFE 159

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 Lp+L++L+L+ N ++ +P++ F+g
 15088 137 LPSLQSLRLDANLISLVPERSFEG 160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sL++L L +N L+ eIP n
 15088 161 LSSLRHLWLDNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031

FIGURE 11 cont.

```

      *->LpnLreLdLsnNqLtsLPpgaFqg<-*
      L++Lr+L L++N+Lt++P +a+++
15088 161 LSSLRHLWLDDNALTEIPVRALNN 184

LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
      *->LtnLeeLdLsqNkI.....kkiENLde<-*
      L+ L++L+L +N +++ + + NL
15088 161 LSSLRHLWLDDNALteipvRALNNLPA 187

LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
      *->npsLreLdLsnNklgdeGaraL..aeaLks<-*
      ++sLr L+L +N l++ +raL++ aL++
15088 161 LSSLRHLWLDDNALTEIPVRALnnLPALQA 190

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
      *->LtsLqvLdLsnNnLsGeIPsslgn<-*
      L+ Lq L+ N++s +IP+ ++
15088 185 LPALQAMTLALNRIS-HIPDYAFQ 207

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
      *->LpnLreLdLsnNqLtsLPpgaFqg<-*
      Lp+L+ L N+++++P+ aFq+
15088 185 LPALQAMTLALNRISHIPDYAFQN 208

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79
      *->LtsLqvLdLsnNnLsGeIPsslgn<-*
      LtsL+vL+L+nN++ s+
15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
      *->LpnLreLdLsnNqLtsLPpgaFqg<-*
      L++L +L+L+nN++++L F+g
15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
      *->npsLreLdLsnNklgdeGaraLaeaLks<-*
      ++sL +L+L nN + G + e+L+
15088 209 LTSLVVLHLHNNRIQHLGTHSF-EGLHN 235

LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
      *->LtnLeeLdLsqNkI.....kkiENLde<-*
      Lt L++L L +N+I++ +++++E+L++
15088 209 LTSLVVLHLHNNRIqhlgtHSFEGLHN 235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
      *->PpsLkeLnvsnNrLteLPeL<-*
      ++L++L+ ++N+L e+P
15088 233 LHNLETLDLNYNKLQEFPA 252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
      *->LpnLreLdLsnNqLtsLPpgaFqg<-*
      L+nL++LdL++N+L++ P + +
15088 233 LHNLETLDLNYNKLQEFPAI-RT 255

LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
      *->LtsLqvLdLsnNnLsGeIPsslgn<-*
      L++L++LdL++N+L e+P +
15088 233 LHNLETLDLNYNKLQ-EFPVAIRT 255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
      *->PpsLkeLnvsnNrLteLPeL<-*
      +L+eL+ nN+++ Pe
15088 256 LGRLQELGFHNNNIKAIPK 275

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
      *->LtsLqvLdLsnNnLsGeIPsslgn<-*
      L +Lq+L ++nNn+ IP+ +
15088 256 LGRLQELGFHNNNIK-AIPEKAFM 278

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
      *->LpnLreLdLsnNqLtsLPpgaFqg<-*

```

FIGURE 11 cont.

15088 256 L+ L+eL +nN++++P+ aF g
 LGR LQELGFHNNNIKA IPEKAFMG 279
 LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 ++L+ L L + ++ LP+g++q
 15088 327 TTSLEILT LTRAGIRLLPSGMCQQ 350
 LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
 ->PpsLkeLnvsNnrLteLPeL<-
 p+L+ L s+N+++eLP L
 15088 351 LPRLRVLELSHNQIEELPSL 370
 LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L++L+vL+Ls+N++ e+Ps l +
 15088 351 LPRLRVLELSHNQIE-ELPS-LHR 372
 LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
 ->LtnLeeLdLsqNkIkkiENLde<-
 L +L++L+Ls+N+I+ + L+
 15088 351 LPRLRVLELSHNQIEELPSLHR 372
 LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 Lp Lr+L Ls+Nq+++LP + +++
 15088 351 LPRLRVLELSHNQIEELP-SLHRC 373
 LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
 ->npsLreLdLsnNklgdeGaraLaealks<-
 +p+Lr+L Ls+N + + + ++ L++
 15088 351 LPRLRVLELSHNQIEELPSLHRCQKLEE 378
 LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 +++L+++ L++N++ +++++
 15088 373 CQKLEEIGLQHNRIWEIGADTFSQ 396
 LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 +L+e L++N++ ++ +++F+
 15088 374 -QKLEEIGLQHNRIWEIGADTFSQ 396
 LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
 ->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdLs+N I+++
 15088 397 LSSLQALDLSWNAIRSIHPEAF 418
 LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L+sLq LdLs+N + +I ++ ++
 15088 397 LSSLQALDLSWNAIR-SIHPEAFS 419
 LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L++L+ LdLs+N+++++p+aF+
 15088 397 LSSLQALDLSWNAIRSIHPEAFST 420
 LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
 ->PpsLkeLnvsNnrLteLPeL<-
 +sL +L+ +N+Lt+LP
 15088 421 LHSLVKLDLTDNQLTTLPLA 440
 LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
 ->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdL +N+++ + L +
 15088 421 LHSLVKLDLTDNQLTTL-PLAG 441
 LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L+sL+ LdL +N+L+ ++P g

FIGURE 11 cont.

```

15088  421  LHSLVKLDLTDNQLT-TLPL-AGL      442
LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
          *->LpnLreLdLsnNqLtsLPpgaFqg<-*
          L++L +LdL +NqLt+LP      ++g
15088  421  LHSLVKLDLTDNQLTTLPPLAGLGG    444
//

```

FIGURE 11 cont.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87														

mLGR6 - 1 (analysis only) - Import - complete

to: FrGcgManager_101_ITA0fLsO_ check: 3059 from: 1 to: 2711

corrected human LGR6 (analysis o - Import - complete

```
Symbol comparison table:
/ddm_local/gcgc/gcgc_9.1/gcgc/core/data/rundata/nwsgapdna.cmp
CompCheck: 8760
```

```

Gap Weight:      12      Average Match: 10.000
Length Weight:   . 4     Average Mismatch: 0.000

```

Quality:	21826	Length:	3688
Ratio:	8.051	Gaps:	20
Percent Similarity:	84.248	Percent Identity:	84.211

Match display thresholds for the alignment(s):

$I = \text{IDENTITY}$

$$: = 5$$
$$\cdot = 1$$

```
FrGcgManager 101 HTAUB3ha_ x FrGcgManager_101_ITA0fLsO_
```

901	CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACCTAT	950	MOUSE
1GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT	36	HUMAN
951	AATGAGCTGCAGGAGTTCCCCTTGGCTATCCGGACCCTGGGCAGACTGCA	1000	
37	AACAAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA	86	
1001	AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT	1050	
87	GGAAGTGGGGTTCCATAACAACAACATCAAGGCCATCCCAGAAAAGGCCT	136	
1051	TCATGGGCAACCCTCTCCTGCAGACAATACATTTTTATGACAACCCAATC	1100	
137	TCATGGGGAACCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC	186	
1101	CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACGCT	1150	
187	CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT	236	
1151	ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCCAGACCTCAAAGGCA	1200	
237	ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA	286	
1201	CCACTAGCCTGGAGATCCTGACCCTGACCCGTGCGGGCATCAGACTGCTC	1250	
287	CCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTC	336	
1251	CCACCGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC	1300	
337	CCATCGGGGATGTGCCAACAGCTGCCAGGCTCCGAGTCTGGAACTGTC	386	

FIGURE 12

1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG 1350
 ||| ||||| || ||||| | ||||| ||||| ||||| |||
 387 TCACAATCAAATTGAGGAGCTGCCCAGCCTGCACAGGTGTCAGAAATTGG 436
 1351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
 ||||| ||||| || ||| ||| ||||| || ||| |||
 437 AGGAAATCGGCCTCCAACACAACCGCATCTGGGAAATTGGAGCTGACACC 486
 1401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT 1450
 ||||| ||||| ||||| || || || || ||||| |||||
 487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT 536
 1451 CCGTGCCATCCACCCTGAGGCCTTCTCAACCCTTCGATCCTTGGTTAAGC 1500
 ||| ||||| ||||| ||||| ||||| | ||| ||||| |||||
 537 CCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAAGC 586
 1501 TGGACCTGACTGACAACCAGCTGACCACACTGCCCCCTGGCTGGGCTGGGA 1550
 ||||| ||||| ||||| ||||| ||||| || |||
 587 TGGACCTGACAGACAACCAGCTGACCACACTGCCCCCTGGCTGGACTTGGG 636
 1551 GGCCTGATGCACCTGAAGCTCAAAGGGAACCTTGGCCCTGTCTCAGGCCTT 1600
 ||| ||||| ||||| ||||| ||||| || ||| || ||||| |||||
 637 GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCTT 686
 1601 CTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCCTACGCCT 1650
 ||||| ||||| ||||| ||||| ||||| || ||| || ||||| |||||
 687 CTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCT 736
 1651 ACCAGTGCTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGG 1700
 ||||| ||||| ||||| || || || ||||| ||||| ||||| |||||
 737 ACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG 786
 1701 CAGTGGCAGGCCGAGGACTTTCATCCAGAAGAAGAGGAGGCACCAAAGAG 1750
 ||||| ||||| || ||| ||||| | || || ||||| | ||||| |||
 787 CAGTGGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAAG 836
 1751 GCCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC 1800
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 837 GCCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACC 886
 1801 TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCAGTGTC 1850
 ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
 887 TGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCAGTGTC 936
 1851 CAGTGCAGCCCTGTTCCAGGCCCTTCAAGCCCTGCGAGCACCTCTTTGA 1900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 937 CAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGA 986
 1901 GAGCTGGGGCATCCGCCTTGCTGTGTGGGCCATCGTGCTGCTCTCCGTAC 1950
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 987 AAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGC 1036
 1951 TCTGTAACGGGCTGGTGCTGCTGACAGTCTTTGCCAGCGGACCCAGCCCCG 2000
 |||| || || ||||| ||||| || || || ||||| || |||
 1037 TCTGCAATGGACTGGTGCTGCTGACCGTGTTGCTGGCGGGCCTGCCCCC 1086
 2001 CTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAACGCCCT 2050
 ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1087 CTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAACACCTT 1136

FIGURE 12
 CONT.

2051	GACGGGCATTTCTGTGGTCTCCTGGCCCTCTGTGGACGCCCTTGACCTATG	2100
1137	GACTGGCATTTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTG	1186
2101	GTCAGTTCGCTGAGTATGGAGCCCCTGGGAGAGCGGTCTGGGCTGCCAG	2150
1187	GTCAGTTCTCTGAGTACGGAGCCCCTGGGAGACGGGGCTAGGCTGCCGG	1236
2151	GCTACGGGGCTTCTGGCTGTCTGGGTTCAGAGGCGTCGGTGCTGCTGCT	2200
1237	GCCACTGGCTTCTGTGCAGTACTTGGGTCTGGAGGCATCGGTGCTGCTGCT	1286
2201	CACACTGGCGGCCGTGCAGTGCAGCATCTCTGTGACCTGCGTCCGAGCCT	2250
1287	CACTCTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCT	1336
2251	ACGGGAAGGCGCCGTGCCTGGCAGCGTCCGCGCAGGCGCACTGGGATGC	2300
1337	ATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGCTGC	1386
2301	CTGGCGCTGGCCGGGCTGGCCGCAGCACTGCCCTGGCCTCGGTGGGAGA	2350
1387	CTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCTGGCCTCAGTGGGAGA	1436
2351	GTATGGCGCCTCCCCACTCTGCCTGCCCTACGCCCCACCCGAGGGCCGGC	2400
1437	ATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCAGC	1486
2401	CGGCCGCCCTGGGCTTCGCTGTAGCCCTGGTGATGATGAACCTCGCTCTGC	2450
1487	CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCCTTCTGT	1536
2451	TTCCTGGTGGTGGCCGGCGCCTACATCAAGCTCTACTGTGACCTGCCACG	2500
1537	TTCCTGGTCGTGGCCGGTGCCTACATCAAACCTGTACTGTGACCTGCCGCG	1586
2501	GGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGGCCT	2550
1587	GGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCT	1636
2551	GGCTCATCTTTGAGATGGCCTCCTCTACTGCCCCGTGGCCTTCCTCAGC	2600
1637	GGCTCATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGC	1686
2601	TTTGCTCCATGCTGGGCCTCTTCCCTGTACCCCCGAGGCTGTCAAGTC	2650
1687	TTGCTCCATGCTGGGCCTCTTCCCTGTACGCCCCGAGGCCGTCAAGTC	1736
2651	AGTCCTTCTGGTGGTGCTGCCTCTGCCTGCCTGCCTCAACCCACTGCTCT	2700
1737	TGTCCTGCTGGTGGTGCTGCCCTGCCTGCCTGCCTCAACCCACTGCTGT	1786
2701	ACCTGCTCTTCAACCCTCACTTCCGGGATGACCTTCGGCGGCTCTGGCCA	2750
1787	ACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCC	1836
2751	AGCCCTCGGTCCCCAGGGCCCCCTAGCCTACGCTGCAGCCGGTGAGCTGGA	2800
1837	CGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGA	1886

FIGURE 12
CONT.

2801 GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTTCTCAGATGTGG 2850
 ||||| || || ||||| || ||||| || ||||| |||||
 1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG 1936
 2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC 2900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1937 ATCTCATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACC 1986
 2901 TATGGCTTCCCTTCAGTGACCCCTCATCTCCCGACATCAGCCGGGGGCCAC 2950
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1987 TATGGCTTCCCTTCAGTGACCCCTCATCTCCTGTCAGCAGCCAGGGGCCCC 2036
 2951 CAGGCTGGAGGGAAACCATTTTATAGAGTCTGATGGAACCAAGTTTGGGA 3000
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2037 CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086
 3001 ACCCACAACCTCCCATGAAGGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC 3050
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2087 ACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT 2136
 3051 ACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCCCTCTGGCCCTCTGG 3100
 || ||||| || ||||| || ||||| || ||||| ||||| |||||
 2137 ACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTTAGCCCTCTGG 2186
 3101 CTCTCTCTTTGCCTCTCACTTGTAATATCCCT..... 3133
 || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 2187 CTTGGCCTTTGCTTCACACGTGTAATATCCCTCCCCATTCTTCTCTTCC 2236
 3134 .CTCTGTT...TGTC..CTCTCCCCATC...CAATGATGGCTGCTTATAA 3174
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2237 CCTCTCTTCCCTTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA 2286
 3175 AAGAAAGACAACCTCCAAC.....TCCATAGCAAGATGGCCAAC 3212
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2287 AACAAATACAACCAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAG 2336
 3213 ACCTCTGACTCCATTGTT...CTCTCTCCACGACCCCTAACCAATGAGTG 3259
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2337 TAC.CTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGTG 2385
 3260 CTTCCAAGTCTTGCTTTGTCTTGGCCT...TCAGCTTCACTTTCACCCCTG 3306
 || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2386 CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTACCTTGATACTG 2435
 3307 GGC..CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT 3353
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2436 GGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT 2485
 3354 ...TGCATAGGAGAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGC 3400
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2486 GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAG.....GGG. 2527
 3401 CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA 3449
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2528 ..TG...GAGGGTTGATC....AGGGCACAGTGGACAGGGAGACCTCACA 2568
 3450 GAGCATGACACTGGAAGACAACCTACCAAAGACATTGGAGAGTCTCCCCTG 3499
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2569 GAGAAAGGC.CTGAAGGTGATTTC.....CGTGTGACTC..... 2603

FIGURE 12

CONT.

Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	18	65	32	28	38	30	0.15	2.1	0.98	Normal
Gender	1.2	0.4	1	2	1	1	1	1	0.05	0.2	0.99	Normal
Education	12.5	2.1	9	16	12	11	13	12	0.12	1.8	0.97	Normal
Income	1500	500	500	3000	1200	800	1800	1000	0.25	3.5	0.95	Normal
Marital Status	1.5	0.5	1	2	1	1	1	1	0.08	0.3	0.99	Normal
Occupation	2.5	1.2	1	4	2	1	3	2	0.18	2.5	0.96	Normal
Health Status	1.8	0.6	1	2	1	1	1	1	0.02	0.1	0.99	Normal
Stress Level	3.2	1.5	1	5	3	2	4	3	0.10	2.0	0.97	Normal
Life Satisfaction	4.5	1.0	3	5	4	4	4	4	0.01	0.0	0.99	Normal
Resilience	2.8	1.2	1	4	3	2	3	3	0.12	2.2	0.96	Normal
Optimism	3.8	1.1	2	5	4	3	4	4	0.05	0.5	0.99	Normal
Emotional Stability	2.2	0.8	1	3	2	1	2	2	0.08	0.8	0.98	Normal
Self-Esteem	3.5	1.0	2	4	3	3	3	3	0.03	0.1	0.99	Normal
Life Purpose	3.0	1.2	1	4	3	2	3	3	0.15	2.5	0.95	Normal
Gratitude	4.0	1.0	3	5	4	4	4	4	0.01	0.0	0.99	Normal
Forgiveness	3.5	1.1	2	4	3	3	3	3	0.05	0.5	0.99	Normal
Empathy	3.2	1.0	2	4	3	3	3	3	0.02	0.1	0.99	Normal
Resilience	2.8	1.2	1	4	3	2	3	3	0.12	2.2	0.96	Normal
Optimism	3.8	1.1	2	5	4	3	4	4	0.05	0.5	0.99	Normal
Emotional Stability	2.2	0.8	1	3	2	1	2	2	0.08	0.8	0.98	Normal
Self-Esteem	3.5	1.0	2	4	3	3	3	3	0.03	0.1	0.99	Normal
Life Purpose	3.0	1.2	1	4	3	2	3	3	0.15	2.5	0.95	Normal
Gratitude	4.0	1.0	3	5	4	4	4	4	0.01	0.0	0.99	Normal
Forgiveness	3.5	1.1	2	4	3	3	3	3	0.05	0.5	0.99	Normal
Empathy	3.2	1.0	2	4	3	3	3	3	0.02	0.1	0.99	Normal

CONT .

GAP of: FrGcgManager_102_MTA0uXMaE check: 8470 from: 1 to: 968

mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAf7nC1_ check: 5092 from: 1 to: 737

corrected hLGR6.aa (analysis onl - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62

CompCheck: 1102

Matrix made by matblas from blosum62.iiij

Gap Weight: 12 Average Match: 2.778
Length Weight: 4 Average Mismatch: -2.248

Quality: 3424 Length: 968
Ratio: 4.646 Gaps: 0
Percent Similarity: 90.773 Percent Identity: 89.281

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nC1_

201 IPDYAFQNLTSLVVLHLHNNRIQHVGTSHFEGLHNLETLDLNYNELQEFF 250 MOUSE
1GLHNLETLDLNYNKLQEFF 19 HUMAN
251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
20 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69
301 FQYLSKLHTLSLNGATDIQEFDPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
70 FQYLPKLHTLSLNGAMDIEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 119
351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169
401 QALDLSWNAIRAIHPEAFSTLRSVLKLDLTDNQLTTLPLAGLGGLMHLKL 450
170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 219
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSQWQAEDF 500
220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 269
501 HPEEEEEAPKRPLGLLAGQAENHYDLDELQMGTEDESKPNPSVQCSPVPG 550
270 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 319
551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLV 600
320 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 369

FIGURE 13

>15088
> Fbh150881 - Import - vector trimmed
CCGCCSGCGGTGCAGCCCGCCGGGACCGGGAGGCGGCAGCTGCGGCCACCGCGCCGTGCG
TCCGCGCCCGGCCCGCCAGGTGCCCGAGTAGCCCGACCGCCGAGATGCCAGCCCGCCGGG
GCTCCGGGCGCTATGGCTTTGCGCCGCGCTGTGCGCTTCCCGGAGGGCCGCGCGGCCCC
CCAGCCCGGGCCCGGGGCCACCGCCTGCCCGGCCCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGGCTGTCCGCCGTTCCGGGGGACCTGGACCC
CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT
CCACCACCTGCGCTTCTTGAGGAGCTGCGTCTCTTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGGTCTCTACAGCCTGAAAACTCTGATGCTGCAGAACAATCAGCT
GGGAGGAATCCCCGAGAGGCGCTGTGGGAGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA
TGCCAACCTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCTCCCTCCCGCCA
CCTCTGGCTGGACGACAATGCACTCACGGAGATCCCTGTCAGGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCTGGCCCTCAACCGCATCAGCCACATCCCCGACTACGCGTT
CCAGAATCTCACCAGCCTTGTGGTGTGCAATTTGCATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGATCTCCCTGTGGCCATCCGGACCTGGGCAGACTGCAGGAACTGGGGTTCCATAA
CAACAACATCAAGGCCATCCAGAAAAGGCCTTCATGGGGAACCTCTGCTACAGACGAT
ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG
GATGTGCCAACAGCTGCCAGGCTCCGAGTCTGGAAGTGTCTACAATCAAATTGAGGA
GCTGCCCAGCCTGCACAGGTGTGAGAAATTGGAGGAAATCGGCCCTCAACACAACCGCAT
CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCCTCGGTCCATCCACCTGAGGCCCTTCTCCACCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCC
AAAAGTGAAGATCCTGGAGGTGCCTTATGCCTACCAAGTGTGTCCCTATGGGATGTGTGC
CAGCTTCTTCAAGGCCTTGGGCAGTGGGAGGCTGAAGACCTTCACTTGATGATGAGGA
GTCTTCAAAAAGGCCCTGGGCCCTCTTGCCAGACAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCACTGTCCAGTGTAG
CCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTGAAGCTGGGGCATCCGCCT
GGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTGCAATGGAGTGGTGTGCTGCTGACCGT
GTTGCTGGCGGGCCTGCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAACACCTTGACTGGCATTCTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTCTGAGTACGGAGCCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGG
CTTCTTGGCAGTACTTGGGTCCGAGGCATCGGTGCTGCTGCTCACTTGGCCGCAATGCA
GTGCAAGCGTCTCCGTCTCTGTGTCCGGGCCATGGGAAGTCCCCCTCCCTGGGCAGCGT
TCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCGCACTGCCCTGGC
CTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCCTGCCCTACGCGCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTCAACCGTGGCCCTGGTGATGATGAAGTCTTCTGTTTCTGGT
CGTGGCCGGTCCCTACATCAAAGTGTACTGTGACCTGCCGCGGGGCACTTTGAGGCCGT
GTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGACAGCGGGCTCCTCTA
CTGTCCCGTGGCCTTCTCAGCTTCGCCCTCCATGCTGGGCCTTCCCTGTACGCCCCGA
GGCCGTCAAAGTCTGTCTGTGGTGGTGTGCCCTGCCTGCCTGCCTCAACCACTGCT
GTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGCAGG
GGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGCTCCTGTGATTC
TACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGG
GCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCTCATCTCCTGTACGCA
GCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG
GAACCCCCAACCTCCATGGATGGAGAAGTGTGCTGAGGGCAGAGGGATCTACGCCAGC
AGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGTCTCACA
CGTGTAAATATCCCTCCCCATTCTTCTTCCCCTCTTCCCTTCTCTCTCCCCCTC
GGTGAATGATGGCTGCTTCTAAAACAAATACAACCAAACTCAGCAGTGTGATCTATAGC
AGGATGGCCCACTACCTGGCTCCACTGATCACCTCTCTCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCTTCCCTTGGCCTTCTCAGCTTACCTTGATACTGGGCCTCTTC
CTGTGCATGTCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA
GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCT
CACARAAAAAGGCCTGGAAGGKATTTCCCGTGTGACTCATGGRTAGGAWACAAATGTG
TTCCATGTACCATTAATCTTGACATATGCCATGCATAAARACTTCTATTAAAATAAGCT
TTGGRAGAGATT

FIGURE 14

>15088
MPSPPPGLRALWLCAALCASRRAGGAPQPGPGPTACAPCHCQEDGIMLSADCSSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPGFLHHLRFLLEELRLSGNHLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
LSRHLWLDDNALTEIPVRALNNPALQAMTLALNRISHIPDYAFQNLTSVLVHLHNNRIQHLGTHSFEGHLNLETLDLNYNK
LQEFPAVIRTLGRLQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSAFYQLPKLHTLSNGAMDQIEFPDLKGT
SLEILTLAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEIGLQHNRWEIGADTFYQSSSLQALDSLWNAIR
SIHPEAFSTLHSLVKLDDLTDNLTLPLAGLGLMLHLKGNLALQSAFSKDFPKLRIVEVPYAYQCCPYGMCASFFKASG
QWEAEDLHLDDEESSKRPLGQLLARQANENHYDQDLDELQLEMEDSKPHSPVQCSPTPGPFKPCEYLFESWGIRLAWVAIVL
LSVLCNGLVLLTVFAGGPAPLPVVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSE
ASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLAGLAAALPLASVGEYGFASMLCLPYAPPEGQPAALGFTVA
LVMMNSFCFLVWAGAIYIKLYCDLPRGDFEAWWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGLFPVTPTEAVKSVLLVLV
PLPACLNPLLYLLFNPHFRDDLRLRLPRAGDSGLAYAAAGELEKSSCDTQALVAFSDVDLILEASEAGRPPGLETYGFP
SVTLISCQQPQAPRLEGSHCVEPEGNHFGNPPQPSMDGELLRLAEGSTPAGGGLSGGGGFQPSGLAFASHV*

[illegible]

